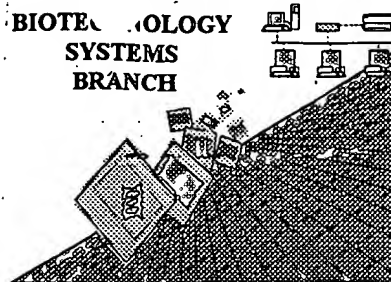


9/1/00

RAW SEQUENCE LISTING
ERROR REPORT



P#20

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/164,862A
Source: 1642
Date Processed by STIC: 12/6/2000

RECEIVED

DEC 19 2000

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING DATE: 12/06/2000
PATENT APPLICATION: US/09/164,862A TIME: 13:10:40

Input Set : A:\PTO.txt
Output Set: N:\CRF3\12062000\I164862A.raw

Does Not Comply
Corrected Diskette Needed

```

5 <110> APPLICANT: Price, Paul A
6 Johansen, Julia S
10 <120> TITLE OF INVENTION: YKL-40 AS A MARKER AND PROGNOSTIC INDICATOR FOR CANCERS
14 <130> FILE REFERENCE: 2500.121US0
18 <140> CURRENT APPLICATION NUMBER: 09/164,862A
20 <141> CURRENT FILING DATE: 1998-10-01
24 <160> NUMBER OF SEQ ID NOS: 4
28 <170> SOFTWARE: PatentIn Ver. 2.0
32 <210> SEQ ID NO: 1
34 <211> LENGTH: 25
36 <212> TYPE: PRT
38 <213> ORGANISM: Artificial Sequence see item 12 on Evan Sum
42 <220> FEATURE:
44 <221> NAME/KEY: UNSURE
46 <222> LOCATION: (20)
48 <223> OTHER INFORMATION: Xaa - RESIDUE UNSURE
52 <400> SEQUENCE: 1
54 Tyr Lys Leu Val Cys Tyr Tyr Thr Ser Trp Ser Gln Tyr Arg Glu Gly
56 1 5 10 15
60 Asp Gly Ser Xaa Phe Pro Asp Ala Leu
62 20 25
68 <210> SEQ ID NO: 2
70 <211> LENGTH: 19
72 <212> TYPE: PRT
74 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
80 <223> OTHER INFORMATION: Description of Artificial Sequence: An internal
82 amino acid sequence for the YKL-40 protein (YKL-40
84 peptide A).
88 <400> SEQUENCE: 2
90 Leu Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu Ser
92 1 5 10 15
96 Val Gly Gly
104 <210> SEQ ID NO: 3
106 <211> LENGTH: 7
108 <212> TYPE: PRT
110 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence: YKL-40 peptide
118 B.
122 <400> SEQUENCE: 3
124 Leu Arg Leu Gly Ala Pro Ala
126 1 5
132 <210> SEQ ID NO: 4
134 <211> LENGTH: 1681
136 <212> TYPE: DNA
138 <213> ORGANISM: Artificial Sequence

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RECEIVED

DEC 19 2003

TECH CENTER 1600/2900

RAW SEQUENCE LISTING DATE: 12/06/2000
 PATENT APPLICATION: US/09/164,862A TIME: 13:10:40

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\12062000\I164862A.raw

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142 <220> FEATURE:
144 <223> OTHER INFORMATION: Description of Artificial Sequence:cDNA nucleotide
146     sequence for the coding region of the gene for
148     YKL-40.
152 <400> SEQUENCE: 4
154 ctaggtagct ggcaccagga gccgtgggca agygaagagg ccacaccctg cctgctctcg 60
156 ctgcagccag aatgggtgtg aagqcgcttc aaacaqctt tgtggtccty qtgctgctcc 120
158 agtqctgctc tgcatacaaa ctggtctgct actacaccag ctggtcccaq taccgggaag 180
160 gcgatgggag ctgcttccca gatgcccttg accgcttcct gtgtaccac atcatctaca 240
162 gctttgccaa tataagcaac gatacactcg araccctyga gtggaatgat gtgacgclct 300
164 acggcatgct caacacactc aacaacacga accccaacct gaagactctc ttgtctgtcg 360
166 qaqqatggaa ctttgggtct caaagatttt ccaagatagc ctccaacacc cagagtctgc 420
168 ggactttcat caagtcaqta ccgccatttc tgcgcacca tggctttgat gggcgtgacc 480
170 ttgcctgyct ctaccctgga cggagagaca aacaccattt taccacccta atcaaggaaa 540
172 tgaagggcga atttataaaq gaagcccagc cagggaaaaa gcaqctcctg ctcaqcgcaq 600
174 cactgtcttc qggqaaqgtc accattqaca qcaqctatga cattgccaaq atatcccaac 660
176 acctggattt cattagcctc atgacctacg attttcatgg cgcctggcgt gggaccacag 720
178 gccatcacag tccctcagg cggggtcagg aggatqcaa tcttgacaga ttcaagcaaca 780
180 ctgactatgc tgtgggttac atgttgaggc tgggggctcc tgcagtaag ctggtgatgg 840
182 gcatccccc ctctgggaag agcttcactc tggcttcttc tgaqactggt gtccaagcgc 900
184 caatctcagg accgggaatt ccaggccggt tcaccaagga ggcagggacc cttgcctact 960
186 atgagatctg tgaacttctc cgcggagcca caqtccatag aacctctggc cagcaggctc 1020
188 cctatgccac caaggqcaac caqtgggtag qatcacqaca ccaggaaagc gtcaaaaaga 1080
190 aggtgcagta cctgaaggat aggcagctgg caggcgccat ggtalggcc ctggacctgg 1140
192 atgacttcca ggcctccttc tgcggccagg atctgcctt cctctcacc aatqccatca 1200
194 aggatgcact cgtgcaacg tagccctctg ttctgcacac agcacggggg ccaaggatgc 1260
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198 cctcagcttc cctcccttgg ggcctatgca gaggtccaca acacacagat ttgaqctcaq 1380
200 cctggtggg cagagaggta cacacttgtt gatgatttat ggaaatgttt acagatcccc 1440
202 aagcctggca agggaatttc ttcaactccc tgcacctag cctctcttat caaaggcac 1500
204 cattttggca agctctatca ccaaggagcc aaacatccta caagacacag tgaccatact 1560
206 aattataccc cctgcaaaag cagcttqaaa ccttcactta qqaacgtaat cgtatccct 1620
208 atcctacttc ccttctctaa ttccacagct gctcaataaa gtacaagagt ttaacagtyt 1680
210 g                                     1681

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/164,862A

DATE: 12/06/2000

TIME: 13:10:41

Input Set : A:\PTO.txt

Output Set: N:\CRF3\12062000\I164862A.raw

L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/164,862A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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To Purchase PatentIn Software.....703-306-2600

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